

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/586,229
Source: 1FwP
Date Processed by STIC: 7/26/06

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IFWP

RAW SEQUENCE LISTING

PATENT APPLICATION: US/10/586,229

DATE: 07/26/2006

TIME: 14:17:48

Input Set: A:\50274.021003.SEQLIST.TXT
 Output Set: N:\CRF4\07262006\J586229.raw

4 <110> APPLICANT: VOLLMERS, Heinz Peter
 5 MUELLER-HERMELINK, Hans Konrad
 6 HENSEL, Frank
 8 <120> TITLE OF INVENTION: Neoplasm-Specific Polypeptides and Their
 9 Uses
 11 <130> FILE REFERENCE: 50274/021003
 C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/586,229
 C--> 13 <141> CURRENT FILING DATE: 2006-07-19
 13 <150> PRIOR APPLICATION NUMBER: PCT/US05/02480
 14 <151> PRIOR FILING DATE: 2005-01-26
 16 <150> PRIOR APPLICATION NUMBER: US 10/764,730
 17 <151> PRIOR FILING DATE: 2004-01-26
 19 <160> NUMBER OF SEQ ID NOS: 30
 21 <170> SOFTWARE: FastSEQ for Windows Version 4.0
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 288
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Mus musculus
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (1)...(288)
 32 <400> SEQUENCE: 1
 33 tcc tgc aag gct tct ggc tac acc ttc act gac tac tat ata aac tgg 48
 34 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn Trp
 35 1 5 10 15
 37 gtg aag cag agg act gga cag ggc ctt gag tgg att gga gag att tat 96
 38 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
 39 20 25 30
 41 cct gga agt ggt aat act tac tac aat gag aag ttc aag ggc aag gcc 144
 42 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
 43 35 40 45
 45 aca ctg act gca gac aaa tcc tcc agc aca gcc tac atg cag ctc agc 192
 46 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
 47 50 55 60
 49 agc ctg aca tct gag gac tct gca gtc tat ttc tgt gca aga tcg gga 240
 50 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
 51 65 70 75 80
 53 tta cga ccc tat gct atg gac tac tgg ggt caa gga acc tca gtc acc 288
 54 Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
 55 85 90 95
 59 <210> SEQ ID NO: 2
 60 <211> LENGTH: 96
 61 <212> TYPE: PRT

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62 <213> ORGANISM: Mus musculus
 64 <400> SEQUENCE: 2
 65 Ser Cys Lys Ala Ser Gly Tyr Thr Phe Thr Asp Tyr Tyr Ile Asn Trp
 66 1 5 10 15
 67 Val Lys Gln Arg Thr Gly Gln Gly Leu Glu Trp Ile Gly Glu Ile Tyr
 68 20 25 30
 69 Pro Gly Ser Gly Asn Thr Tyr Tyr Asn Glu Lys Phe Lys Gly Lys Ala
 70 35 40 45
 71 Thr Leu Thr Ala Asp Lys Ser Ser Ser Thr Ala Tyr Met Gln Leu Ser
 72 50 55 60
 73 Ser Leu Thr Ser Glu Asp Ser Ala Val Tyr Phe Cys Ala Arg Ser Gly
 74 65 70 75 80
 75 Leu Arg Pro Tyr Ala Met Asp Tyr Trp Gly Gln Gly Thr Ser Val Thr
 76 85 90 95
 79 <210> SEQ ID NO: 3
 80 <211> LENGTH: 315
 81 <212> TYPE: DNA
 82 <213> ORGANISM: Mus musculus
 84 <220> FEATURE:
 85 <221> NAME/KEY: CDS
 86 <222> LOCATION: (1)...(315)
 88 <400> SEQUENCE: 3
 89 cca ctc tcc ctg cct gtc agt ctt gga gat caa gcc tcc atc tct tgc 48
 90 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys
 91 1 5 10 15
 93 aga tct agt cag agc att gta cat agt aat gga aac acc tat tta gaa 96
 94 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 95 20 25 30
 97 tgg tac ctg cag aaa cca ggc cag tct cca aag ctc ctg atc tac aaa 144
 98 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 99 35 40 45
 101 gtt tcc aac cga ttt tct ggg gtc cca gac agg ttc agt ggc agt gga 192
 102 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 103 50 55 60
 105 tca ggg aca gat ttc aca ctc aag atc agc aga gtg gag gct gag gat 240
 106 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 107 65 70 75 80
 109 ctg gga gtt tat tac tgc ttt caa ggt tca cat gtt ccg tac acg ttc 288
 110 Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe
 111 85 90 95
 113 gga ggg ggg acc aag ctg gaa ata aaa 315
 114 Gly Gly Gly Thr Lys Leu Glu Ile Lys
 115 100 105
 118 <210> SEQ ID NO: 4
 119 <211> LENGTH: 105
 120 <212> TYPE: PRT
 121 <213> ORGANISM: Mus musculus
 123 <400> SEQUENCE: 4
 124 Pro Leu Ser Leu Pro Val Ser Leu Gly Asp Gln Ala Ser Ile Ser Cys

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125 1 5 10 15
 126 Arg Ser Ser Gln Ser Ile Val His Ser Asn Gly Asn Thr Tyr Leu Glu
 127 20 25 30
 128 Trp Tyr Leu Gln Lys Pro Gly Gln Ser Pro Lys Leu Leu Ile Tyr Lys
 129 35 40 45
 130 Val Ser Asn Arg Phe Ser Gly Val Pro Asp Arg Phe Ser Gly Ser Gly
 131 50 55 60
 132 Ser Gly Thr Asp Phe Thr Leu Lys Ile Ser Arg Val Glu Ala Glu Asp
 133 65 70 75 80
 134 Leu Gly Val Tyr Tyr Cys Phe Gln Gly Ser His Val Pro Tyr Thr Phe
 135 85 90 95
 136 Gly Gly Gly Thr Lys Leu Glu Ile Lys
 137 100 105
 140 <210> SEQ ID NO: 5
 141 <211> LENGTH: 3114
 142 <212> TYPE: DNA
 143 <213> ORGANISM: Homo sapiens
 145 <220> FEATURE:
 146 <221> NAME/KEY: CDS
 147 <222> LOCATION: (1)...(3114)
 149 <400> SEQUENCE: 5
 150 gat gtg agg gag cct gaa aat gaa att tct tca gac tgc aat cat ttg 48
 151 Asp Val Arg Glu Pro Glu Asn Glu Ile Ser Ser Asp Cys Asn His Leu
 152 1 5 10 15
 154 ttg tgg aat tat aag ctg aac cta act aca gat ccc aaa ttt gaa tct 96
 155 Leu Trp Asn Tyr Lys Leu Asn Leu Thr Thr Asp Pro Lys Phe Glu Ser
 156 20 25 30
 158 gtg gcc aga gag gtt tgc aaa tct act ata aca gag att gaa gaa tgt 144
 159 Val Ala Arg Glu Val Cys Lys Ser Thr Ile Thr Glu Ile Glu Glu Cys
 160 35 40 45
 162 gct gat gaa ccg gtt gga aaa ggt tac atg gtt tcc tgc ttg gtg gat 192
 163 Ala Asp Glu Pro Val Gly Lys Gly Tyr Met Val Ser Cys Leu Val Asp
 164 50 55 60
 166 cac cga ggc aac atc act gag tat cag tgt cac cag tac att acc aag 240
 167 His Arg Gly Asn Ile Thr Glu Tyr Gln Cys His Gln Tyr Ile Thr Lys
 168 65 70 75 80
 170 atg acg gcc atc att ttt agt gat tac cgt tta atc tgt ggc ttc atg 288
 171 Met Thr Ala Ile Ile Phe Ser Asp Tyr Arg Leu Ile Cys Gly Phe Met
 172 85 90 95
 174 gat gac tgc aaa aat gac atc aac att ctg aaa tgt ggc agt att cgg 336
 175 Asp Asp Cys Lys Asn Asp Ile Asn Ile Leu Lys Cys Gly Ser Ile Arg
 176 100 105 110
 178 ctt gga gaa aag gat gca cat tca caa ggt gag gtg gta tca tgc ttg 384
 179 Leu Gly Glu Lys Asp Ala His Ser Gln Gly Glu Val Val Ser Cys Leu
 180 115 120 125
 182 gag aaa ggc ctg gtg aaa gaa gca gaa gaa aga gaa ccc aag att caa 432
 183 Glu Lys Gly Leu Val Lys Glu Ala Glu Glu Arg Glu Pro Lys Ile Gln
 184 130 135 140
 186 gtt tct gaa ctc tgc aag aaa gcc att ctc cgg gtg gct gag ctg tca 480

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187	Val	Ser	Glu	Leu	Cys	Lys	Ala	Ile	Leu	Arg	Val	Ala	Glu	Leu	Ser		
188	145				150				155				160				
190	tcg	gat	gac	ttt	cac	tta	gac	cg	cat	tta	tat	ttt	gct	tgc	cga	gat	528
191	Ser	Asp	Asp	Phe	His	Leu	Asp	Arg	His	Leu	Tyr	Phe	Ala	Cys	Arg	Asp	
192												165	170	175			
194	gat	cg	gag	cgt	ttt	tgt	gaa	aat	aca	caa	gct	ggt	gag	ggc	aga	gtg	576
195	Asp	Arg	Glu	Arg	Phe	Cys	Glu	Asn	Thr	Gln	Ala	Gly	Glu	Gly	Arg	Val	
196												180	185	190			
198	tat	aag	tgc	ctc	ttt	aac	cat	aaa	ttt	gaa	gaa	tcc	atg	agt	gaa	aag	624
199	Tyr	Lys	Cys	Leu	Phe	Asn	His	Lys	Phe	Glu	Glu	Ser	Met	Ser	Glu	Lys	
200												195	200	205			
202	tgt	cga	gaa	gca	ctt	aca	acc	cg	caa	aag	ctg	att	gcc	cag	gat	tat	672
203	Cys	Arg	Glu	Ala	Leu	Thr	Arg	Gln	Lys	Leu	Ile	Ala	Gln	Asp	Tyr		
204												210	215	220			
206	aaa	gtc	agt	tat	tca	ttg	gcc	aaa	tcc	tgt	aaa	agt	gac	ttg	aag	aaa	720
207	Lys	Val	Ser	Tyr	Ser	Leu	Ala	Lys	Ser	Cys	Lys	Ser	Asp	Leu	Lys		
208												225	230	235	240		
210	tac	cg	tgc	aat	gtg	gaa	aac	ctt	ccg	cg	tcg	cgt	gaa	gcc	agg	ctc	768
211	Tyr	Arg	Cys	Asn	Val	Glu	Asn	Leu	Pro	Arg	Ser	Arg	Glu	Ala	Arg	Leu	
212												245	250	255			
214	tcc	tac	ttg	tta	atg	tgc	ctg	gag	tca	gct	gta	cac	aga	ggg	cg	caa	816
215	Ser	Tyr	Leu	Leu	Met	Cys	Leu	Glu	Ser	Ala	Val	His	Arg	Gly	Gln		
216												260	265	270			
218	gtc	agc	agt	gag	tgc	cag	ggg	gag	atg	ctg	gat	tac	cga	cgc	atg	ttg	864
219	Val	Ser	Ser	Glu	Cys	Gln	Gly	Glu	Met	Leu	Asp	Tyr	Arg	Arg	Met	Leu	
220												275	280	285			
222	atg	gaa	gac	ttt	tct	ctg	agc	cct	gag	atc	atc	cta	agc	tgt	cg	ggg	912
223	Met	Glu	Asp	Phe	Ser	Leu	Ser	Pro	Glu	Ile	Ile	Leu	Ser	Cys	Arg	Gly	
224												290	295	300			
226	gag	att	gaa	cac	cat	tgt	tcc	gga	tta	cat	cg	aaa	ggg	cg	acc	cta	960
227	Glu	Ile	Glu	His	His	Cys	Ser	Gly	Leu	His	Arg	Lys	Gly	Arg	Thr	Leu	
228												305	310	315	320		
230	cac	tgt	ctg	atg	aaa	gt	cg	ggg	gag	aag	ggg	aac	ctt	gga	atg	1008	
231	His	Cys	Leu	Met	Lys	Val	Val	Arg	Gly	Glu	Lys	Gly	Asn	Leu	Gly	Met	
232												325	330	335			
234	aac	tgc	cag	cag	g	ctt	caa	aca	ctg	att	cag	gag	act	gac	cct	gg	1056
235	Asn	Cys	Gln	Gln	Ala	Leu	Gln	Thr	Leu	Ile	Gln	Glu	Thr	Asp	Pro	Gly	
236												340	345	350			
238	gca	gat	tac	cgc	att	gat	cg	g	c	tgt	aaa	gct	tgt	gaa	tct	gt	1104
239	Ala	Asp	Tyr	Arg	Ile	Asp	Arg	Ala	Leu	Asn	Glu	Ala	Cys	Glu	Ser	Val	
240												355	360	365			
242	atc	cag	aca	gcc	tgc	aaa	cat	ata	aga	tct	gga	gac	cca	atg	atc	ttg	1152
243	Ile	Gln	Thr	Ala	Cys	Lys	His	Ile	Arg	Ser	Gly	Asp	Pro	Met	Ile	Leu	
244												370	375	380			
246	tcg	tgc	ctg	atg	gaa	cat	tta	tac	aca	gag	aag	atg	gta	gaa	gac	tgt	1200
247	Ser	Cys	Leu	Met	Glu	His	Leu	Tyr	Thr	Glu	Lys	Met	Val	Glu	Asp	Cys	
248												385	390	395	400		
250	gaa	cac	cac	cgt	ctc	tta	gag	ctg	cag	tat	ttc	atc	tcc	cgg	gat	tgg	1248
251	Glu	His	Arg	Leu	Leu	Glu	Leu	Gln	Tyr	Ile	Ser	Arg	Asp	Trp	Lys		

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252	405	410	415	
254	ctg gac cct gtc ctg tac cgc aag tgc cag gga gac gct tct cgt ctt			1296
255	Leu Asp Pro Val Leu Tyr Arg Lys Cys Gln Gly Asp Ala Ser Arg Leu			
256	420	425	430	
258	tgc cac acc cac ggt tgg aat gag acc agc gaa ttt atg cct cag gga			1344
259	Cys His Thr His Gly Trp Asn Glu Thr Ser Glu Phe Met Pro Gln Gly			
260	435	440	445	
262	gct gtg ttc tct tgt tta tac aga cac gcc tac cgc act gag gaa cag			1392
263	Ala Val Phe Ser Cys Leu Tyr Arg His Ala Tyr Arg Thr Glu Glu Gln			
264	450	455	460	
266	gga agg agg ctc tca cgg gag tgc cga gtc gaa gtc caa agg atc cta			1440
267	Gly Arg Arg Leu Ser Arg Glu Cys Arg Ala Glu Val Gln Arg Ile Leu			
268	465	470	475	480
270	cac cag cgt gcc atg gat gtc aag ctg gat cct gcc ctc cag gat aag			1488
271	His Gln Arg Ala Met Asp Val Lys Leu Asp Pro Ala Leu Gln Asp Lys			
272	485	490	495	
274	tgc ctg att gat ctg gga aaa tgg tgc agt gag aaa aca gag act gga			1536
275	Cys Leu Ile Asp Leu Gly Lys Trp Cys Ser Glu Lys Thr Glu Thr Gly			
276	500	505	510	
278	cag aag ctg gag tgc ctt cag gac cat ctg gat gac tta gtg gtg gag			1584
279	Gln Lys Leu Glu Cys Leu Gln Asp His Leu Asp Asp Leu Val Val Glu			
280	515	520	525	
282	tgt aga gat ata gtt ggc aac ctc act gag tta gaa tca gag gat att			1632
283	Cys Arg Asp Ile Val Gly Asn Leu Thr Glu Leu Ser Glu Asp Ile			
284	530	535	540	
286	caa ata gaa gcc ttg ctg atg aga gcc tgt gag ccc ata att cag aac			1680
287	Gln Ile Glu Ala Leu Met Arg Ala Cys Glu Pro Ile Ile Gln Asn			
288	545	550	555	560
290	ttc tgc cac gat gtg gca gat aac cag ata gac tcc ggg gac ctg atg			1728
291	Phe Cys His Asp Val Ala Asp Asn Gln Ile Asp Ser Gly Asp Leu Met			
292	565	570	575	
294	gag tgt ctg ata cag aac aaa cac cag aag gac atg aac gag aag tgt			1776
295	Glu Cys Leu Ile Gln Asn Lys His Gln Lys Asp Met Asn Glu Lys Cys			
296	580	585	590	
298	gcc atc gga gtt acc cac ttc cag ctg gtg cag atg aag gat ttt cgg			1824
299	Ala Ile Gly Val Thr His Phe Gln Leu Val Gln Met Lys Asp Phe Arg			
300	595	600	605	
302	ttt tct tac aag ttt aaa atg gcc tgc aag gag gac gtg ttg aag ctt			1872
303	Phe Ser Tyr Lys Phe Lys Met Ala Cys Lys Glu Asp Val Leu Lys Leu			
304	610	615	620	
306	tgc cca aac ata aaa aag aag gtg gac gtg gtg atc tgc ctg agc acg			1920
307	Cys Pro Asn Ile Lys Lys Val Asp Val Val Ile Cys Leu Ser Thr			
308	625	630	635	640
310	acc gtg cgc aat gac act ctg cag gaa gcc aag gag cac agg gtg tcc			
311	Thr Val Arg Asn Asp Thr Leu Gln Glu Ala Lys Glu His Arg Val Ser			
312	645	650	655	
314	ctg aag tgc cgc agg cag ctc cgt gtg gag gag ctg gag atg acg gag			2016
315	Leu Lys Cys Arg Arg Gln Leu Arg Val Glu Glu Leu Glu Met Thr Glu			
316	660	665	670	

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No

L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date

L:1059 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:26,Line#:1057

L:1099 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:27,Line#:1097